

### In the Claims

Claims 1 – 4 (Canceled)

5. (Currently Amended) The bacterial reverse transcriptase of claim 7, comprising an amino acid sequence selected from the group consisting of SEQ ID NO.: 32, SEQ ID NO.: 33, SEQ ID NO.: 34, SEQ ID NO.: 35, SEQ ID NO.: 37, ~~and SEQ ID NO.: 38, and SEQ ID NO.: 53.~~

6. (Canceled)

7. (Currently Amended) An isolated and purified bacterial reverse transcriptase (RT) which synthesizes msDNA and which is essential for the synthesis of msDNA *in vivo*, said RT comprises a sequence of amino acid residues as recited in SEQ ID NO: 54 follows: ~~Tyr-Xaa<sub>6</sub>-Asp-Asp of SEQ ID NO.: 50, wherein Xaa<sub>6</sub> is alanine or cysteine, wherein said sequence is located in subdomain 5 shown in Fig. 14 at positions 175-191 of SEQ ID NO.: 32, at positions 175-191 of SEQ ID NO.: 33, at positions 175-191 of SEQ ID NO.: 34, at positions 168-184 of SEQ ID NO.: 35, at positions 159-175 of SEQ ID NO.: 36, at positions 171-187 of SEQ ID NO.: 37, and at positions 157-173 of SEQ ID NO.: 38, and further comprising the 61 amino acid residues as indicated by black dots in the consensus sequence shown in Figure 14, wherein h is a hydrophobic residue and p is a small polar residue, wherein said Xaa is any residue, Xaa<sub>0</sub> is any residue or no residue, Xaa<sub>6</sub> is Ala or Cys, Xaa<sub>7</sub> (h) is a hydrophobic residue, Xaa<sub>8</sub> is Lys or Arg, Xaa<sub>9</sub> is Val or Leu, Xaa<sub>10</sub> (p) is a small polar residue, Xaa<sub>11</sub> is Phe or Tyr, Xaa<sub>12</sub> is Val or Phe, Xaa<sub>13</sub> is Met or Phe or Leu, Xaa<sub>14</sub> is Ile or Leu, Xaa<sub>15</sub> is Ser or Thr, Xaa<sub>16</sub> is Ile, Leu or Val and Xaa<sub>17</sub> is Val or Ile.~~

Claims 8 – 18 (Canceled)